

SEQ	ID	NO : 30	MRSYR-FSDYLHMSVSFSNDLFCGEDSGVFSGETVDFSSSEVDSWPGD-----
SEQ	ID	NO : 8	MGDAASTSAPTTPTSI-----LICLEDGSDLADDDGAGTDLVARDERLLVVDQDEE
SEQ	ID	NO : 10	HELTASSS-----LC-----
SEQ	ID	NO : 12	MNAEPPPLPPALLMSVSCLSDYDLLCGEDSSGILSGESPECSESDIDSSPPPSPTTEDCY
SEQ	ID	NO : 14	ARA-----GIM-DSSPECS-SDLDSSPPSEAE-----
		1	60

SEQ	ID	NO : 30	SIACFIEDERHFVPGHDYLSRFQTRSILDASAREDSVAWILKVQAYYNFQPLTAYLAVNYM
SEQ	ID	NO : 8	YVALLLSKESASGGG-GPVEEMEDWM-----KAARSGCVRWIIKTTAMFRFGGKTA YVAVNYL
SEQ	ID	NO : 10	-----WL-----Q-----TNAGFRFSLKTAYVAVTYL
SEQ	ID	NO : 12	SIASFIEHERRNFPVGFEYLSRFQSRSLDANAREEESVGMWILKVHAYYGFQPLTAYLAVNYM
SEQ	ID	NO : 14	SIAGFMEDERNFVPGFEYLNRFQSRSLDASAREEESVAVILKVQAYYYAFQPVTAYLSVNYL
		61	120

SEQ	ID	NO : 30	DRFLIYARRLP-ETSGWPMQLIACLSLAARKMEEILVPSLFDQVAGVKYLPEAKTIKRM
SEQ	ID	NO : 8	DRFLAQRRVNRE-HAWGLQLLMVACMSLATKLEEHAPRILSEFPLDACEFAFDSASILRM
SEQ	ID	NO : 10	DRFLARRCVDRD-KEWALQLLSVACLSLAAKVEERRPRPLPEFKLDM-----YDCASLMRM
SEQ	ID	NO : 12	DRFLDSRRLP-ETNGWPLQLVSVACLSLAARKMEEPLVPSLQLQLEGAKYIFEPRTIRRM
SEQ	ID	NO : 14	DRFLNSRPLPPKTNQGWPLQLLSVACLSLAAKMEESLVPSSLQVEGAKYVFEPKTIRRM
		121	180

SEQ	ID	NO : 30	ELLVLSVLDWRLRSVTPDFDIFISFFAYKIDPSGTFLGFIFSHATEIILSNIKEASFILEYWP
SEQ	ID	NO : 8	ELLVLGTLERMRMIAVTPEPYISYFAARFRETS-----GRILMRAVECVFAAIKVISSVEXRP
SEQ	ID	NO : 10	ELLVLTTLKQMITETPFSYLNCFTAKFRHDER-----KAIVLRAIECIFASIKVISSVGYQP
SEQ	ID	NO : 12	ELLVLGVLIDWRLRSVTPLCFLAFFACKVDTGFLISRATEIIIVSNIQEASFLAYWP
SEQ	ID	NO : 14	ELLVLGVLIDWRLRSVTPFSFLDEFFACKLIDSTGTFITGFLISRATQIILSNIQEASFLAYWP
		181	240

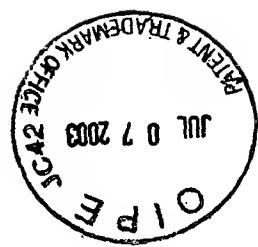


Fig. 2A

SEQ	ID NO: 30	SSIAAAAILCVANELPSLSSVVNPHESSPETWCAGLSKEKIVRCYRLMKAMAIEENRNLNTP
SEQ	ID NO: 8	STIAVASIL-----
SEQ	ID NO: 10	STIALAAIL-----
SEQ	ID NO: 12	SCIAAAAILTAANEIPNWS-VVKP-ENAESWCAGLKEKIVIGCYQLMQUELVINNNQRKLP
SEQ	ID NO: 14	SCIAAAAILHAANEIPNWS-LVRP-EHAESWCAGLKEKIVIGCYQLMQUELVIDNNQRKPP

SEQ	ID NO: 30	--KVIAKL.RVSVRA--	-SSTLTRPSDESSSSP-	-CKRKRKLSGYSWVGDETSNSN
SEQ	ID NO: 8	-	-	-
SEQ	ID NO: 10	-	-	-
SEQ	ID NO: 12	NLDELSVHRLAPWQLMM-	-	-
SEQ	ID NO: 14	LLKVLPQLRVTTTRMRSSSTVSSF--	-SSSSSSTSFSLSCKRKLN	-NNRlwVDD-KGNSE
		-	-	-
		-KVL.PQLRVTTISRPIMRSSVSSFFLASSSSSPSSSSLS	-CRRRKLN	-NNSLWVDDDKGNSQ

Fig. 2B



SEQ ID NO:31
SEQ ID NO:18
SEQ ID NO:22
1
MAADNIYDFVASNILLCTETKS--LCFDDVDSLTIQQNIEETKSKDLSENNNGIRSEPLIDL
MAP-SCYDAASMLCAEEHSSILWYEE-----EEELEAVGRRSGRSRGSPGYGDDFGADL
--
60

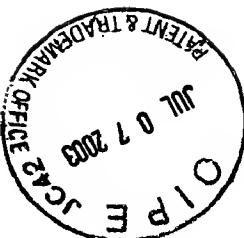
SEQ ID NO:31
SEQ ID NO:18
SEQ ID NO:22
61
-PSLSEECLSFMVQREMEFLPKDDYVERLRSGLDL-SVRKEALDWILKAHMHYGFGELS
FPPQSEECCVAGLVERERDHMPGPCYGDLRGGGCL-CVRREAVDWIWKAYTHHRFRPLT
-----HLRATRGCPVRD-----HPSSDLT
120

SEQ ID NO:31
SEQ ID NO:18
SEQ ID NO:22
121
FCLSINYLDRFLSLYELPRSKTWTVQLLAVACLSLAAKMEEINVPLTVDLQ-VGDPKFVF
AYLAVNYLDRFLSLSEVPDCDKDMMTQQLLAVACVSLAAKMEETAVPQCLDLQEVGDARYVF
ASTIKMXF-----EANSAF
180

SEQ ID NO:31
SEQ ID NO:18
SEQ ID NO:22
181
EGKTIQRMELLVLSTLKWRMQAYTPYTFIDYFMRKMN--GDQIIPSRPLISGSMQLILSII
EAKTVQRMELLVLTTLNWRMHAVTPFSYVDYFLNKLNNNGSTAPRSCWLLQSAELILRAA
EARTIKVMELLVFSSTLKWRMQAVTACSFIDYFLCKFND--HDTPSMLAFSCSTDLLISTT
181

SEQ ID NO:31
SEQ ID NO:18
SEQ ID NO:22
241
RSIDFLEFRSSEIAASVAMSVSGEIQAKDIDKAMP-CFFIHLDKGRVQKCVELIQDLTAA
RGTGCVGFRPSEIAAAAVAAVAGDVIDDADGVENAC-C--AHVDKERVILRCQEAIGSMASS
KXADFLVFRHSEIAGSVALPSFGEHKTSVVEATTNCKYIN---KGWVXCD-----
300

FIG. 3A



SEQ ID NO:31
SEQ ID NO:18
SEQ ID NO:22

TITTAAAASL-----VPQSPIGVLEAAACLSYKSGDERTV-----
AAIDDATVPPKSARRSSPVPVPQSPVGVLDAAPCLSYRSEEATAATSAAASHGAPG
-----RKDPEVLPLW-----NAYLKF-----
301

SEQ ID NO:31
SEQ ID NO:18
SEQ ID NO:22

-----GSCTTSSHTKRRKL-----DTSSLEHGTSEKL
SSSSSSTSPTSKRRKLASRCDGSCSDRSKRAPAQWTKE
-----GLRDML-----
361

FIG. 3B

